```
============================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: markspencer
Timestamp: [year=2010; month=2; day=19; hr=9; min=42; sec=47; ms=323; ]
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*************************************************************
Reviewer Comments:
1.
E355          Empty lines found between the amino acid numbering and
the proteins SEQID ( 11 )
E321          No. of Bases conflict, this line has no nucleotides
SEQID (11) POS (126)
E355          Empty lines found between the amino acid numbering and
the proteins SEQID ( 12 )
E321          No. of Bases conflict, this line has no nucleotides
SEQID (12) POS (0)
E355          Empty lines found between the amino acid numbering and
the proteins SEQID ( 12 )
E321          No. of Bases conflict, this line has no nucleotides
SEQID (12) POS (512)
E355          Empty lines found between the amino acid numbering and
the proteins SEQID ( 22 )
E321          No. of Bases conflict, this line has no nucleotides
SEQID (22) POS (112)
E355          Empty lines found between the amino acid numbering and
the proteins SEQID ( 24 )
E321          No. of Bases conflict, this line has no nucleotides
SEQID (24) POS (496)
E355          Empty lines found between the amino acid numbering and
the proteins SEQID ( 28 )
E321          No. of Bases conflict, this line has no nucleotides
SEQID (28) POS (16)
E355          Empty lines found between the amino acid numbering and
the proteins SEQID ( 30 )
E321          No. of Bases conflict, this line has no nucleotides
SEQID (30) POS (48)
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<210> 11

<211> 1582

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunken-2 gene revertant form

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

* * * * * * * *


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Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
              115                 120                 125


aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act    435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr

        130                 135                 140


tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac    483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
        145                 150                 155
```

For SEQ ID # 11, 12, 22, 24, 28, and 30 the sequence rules specify the numbering for amino acids be placed below the line of amino acids in a protein or coding region of a nucleotide sequence.

"Sec. 1.822 Symbols and format to be used for nucleotide and/or amino acid sequence data.

   (a) The symbols and format to be used for nucleotide and/or amino

acid sequence data shall conform to the requirements of paragraphs (b) through (e) of this section.

(d) Representation of amino acids. (1) The amino acids in a protein or peptide sequence shall be listed using the three-letter abbreviation with the first letter as an upper case character, as in WIPO Standard ST.25 (1998), Appendix 2, Table 3.

(4) The enumeration of amino acids may start at the first amino acid of the first mature protein, with the number 1. When presented, the amino acids preceding the mature protein, e.g., pre-sequences, pro-sequences, pre-pro-sequences and signal sequences, shall have negative numbers, counting backwards starting with the amino acid next to number 1. Otherwise, the enumeration of amino acids shall start at the first amino acid at the amino terminal as number 1. It shall be marked below the sequence every 5 amino acids."

In the SEQ ID numbers listed above there are blank lines found between the amino acids and the numbering for the amino acids at different locations. Please remove all blank lines found between the amino acids and the numbering in these sequences.

2.

E300	Invalid codon found Asn SEQID (11) POS: 388
E300	Invalid codon found Ser SEQID (11) POS: 391
E300	Invalid codon found Gly SEQID (11) POS: 394
E300	Invalid codon found Ile SEQID (11) POS: 397
E300	Invalid codon found Asn SEQID (11) POS: 400
E300	Invalid codon found Lys SEQID (11) POS: 403
E300	Invalid codon found Ile SEQID (11) POS: 406
E300	Invalid codon found Phe SEQID (11) POS: 409
E300	Invalid codon found Val SEQID (11) POS: 412
E300	Invalid codon found Met SEQID (11) POS: 415
E300	Invalid codon found Ser SEQID (11) POS: 418
E300	Invalid codon found Gln SEQID (11) POS: 421
E300	Invalid codon found Phe SEQID (11) POS: 424
E300	Invalid codon found Asn SEQID (11) POS: 427
E300	Invalid codon found Ser SEQID (11) POS: 430
E300	Invalid codon found Thr SEQID (11) POS: 433

The errors shown above are ok and require no response.

* *

Application No: 10569000   Version No: 1.0

                Input Set:

                Output Set:

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                   Finished: 2010-02-18 13:09:51.451
                    Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 957 ms
            Total Warnings: 0
              Total Errors: 302
     No. of SeqIDs Defined: 42
        Actual SeqID Count: 42

Error code   Error Description

E 355   Empty lines found between the amino acid numbering and the

E 321   No. of Bases conflict, this line has no nucleotides   SEQID (11)

E 300   Invalid codon found   Asn SEQID (11)   POS: 388

E 300   Invalid codon found   Ser SEQID (11)   POS: 391

E 300   Invalid codon found   Gly SEQID (11)   POS: 394

E 300   Invalid codon found   Ile SEQID (11)   POS: 397

E 300   Invalid codon found   Asn SEQID (11)   POS: 400

E 300   Invalid codon found   Lys SEQID (11)   POS: 403

E 300   Invalid codon found   Ile SEQID (11)   POS: 406

E 300   Invalid codon found   Phe SEQID (11)   POS: 409

E 300   Invalid codon found   Val SEQID (11)   POS: 412

E 300   Invalid codon found   Met SEQID (11)   POS: 415

E 300   Invalid codon found   Ser SEQID (11)   POS: 418

E 300   Invalid codon found   Gln SEQID (11)   POS: 421

E 300   Invalid codon found   Phe SEQID (11)   POS: 424

E 300   Invalid codon found   Asn SEQID (11)   POS: 427

E 300   Invalid codon found   Ser SEQID (11)   POS: 430

E 300   Invalid codon found   Thr SEQID (11)   POS: 433

E 355   Empty lines found between the amino acid numbering and the

E 321   No. of Bases conflict, this line has no nucleotides   SEQID (12)

```
                    Input Set:


                    Output Set:



                     Started:   2010-02-18 13:09:42.494
                    Finished:   2010-02-18 13:09:51.451
                     Elapsed:   0 hr(s) 0 min(s) 8 sec(s) 957 ms
            Total Warnings:   0
               Total Errors:   302
      No. of SeqIDs Defined:   42
        Actual SeqID Count:   42
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Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (12)
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna

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               This error has occured more than 20 times, will not be displayed
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Input Set:

Output Set:

Started:	2010-02-18 13:09:42.494
Finished:	2010-02-18 13:09:51.451
Elapsed:	0 hr(s) 0 min(s) 8 sec(s) 957 ms
Total Warnings:	0
Total Errors:	302
No. of SeqIDs Defined:	42
Actual SeqID Count:	42

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (24)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (28)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (30)

SEQUENCE LISTING

<110>   University of Florida Research Foundation, Inc.
        Hannah, L. Curtis
        Lyerly Linebarger, Carla R.

<120>   Heat Stable Variants of Adenosine Diphosphate Glucose Pyrophosphorylase

<130>   UF-371XC1 PCT

<140>   10569000
<141>   2010-02-18

<150>   US 60/496,188
<151>   2003-08-18

<160>   42

<170>   PatentIn version 3.2

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<213>   zea mays

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gctcatgata gtgttcttgg aatcattctg ggaggtggtg ctgggactag attgtacccc   180

ttgacaaaga agcgtgccaa gcctgcagtg ccattgggtg ccaactatag actgattgat   240

attcctgtca gcaattgtct caacagcaac atatccaaga tctatgtgct aacgcaattt   300

aactctgctt ccctcaaccg tcacctctca agagcctacg ggagcaacat tggagggtac   360

aagaatgaag ggtttgttga agtcttagct gcacagcaga gcccagataa tccaaactgg   420

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atggaatttc taattcttgc tggcgatcac ctgtaccgga tggactatga aaagttcatt   540

caggcacaca gagaaacaaa tgctgatatt accgttgctg ccctaccgat ggatgagaaa   600

cgtgcaactg catttggcct catgaaaatt gatgaagaag gaggatcat tgagtttgct   660

gagaaaccga aggagagca gttgaaagca atgatggttg acaccaccat acttggcctt   720

gatgacgtga gggcaaagga aatgccttat attgctagca tgggtatcta tgttttcagc   780

aaagatgtaa tgcttcagct cctccgtgaa caatttcctg aagccaatga ctttggaagt   840

gaggttattc caggtgcaac cagcattgga aagagggttc aggcttatct gtatgatggt   900

tactgggaag atatcggtac cattgcggca ttttataatg caaacttggg aataaccaag   960

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aagccaatac cagatttcag cttctatgac cgttttgctc caatttatac acaacctcga    1020

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tgtgttatta aaaactgcaa gataaaccat tctgtagttg gactccgatc ttgcatatct    1140

gaaggtgcta tcatagagga cagtttacta atgggtgcgg actactatga cacagaagct    1200

gataaaaaac tccttgccga aaaaggtggc attcctattg gtattgggaa aaattcatgc    1260

atcaggagag caatcattga caagaatgct cgaattggag acaatgttaa gatactcaat    1320

gctgacaatg ttcaagaagc tgcaatggag acagacgggt acttcatcaa aggtggaatt    1380

gtcacagtga tcaaggatgc tttactccct agtggaacag ttata              1425


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<212>  PRT
<213>  zea mays

<400>  2

Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Trp Asn Ala
1               5                   10                  15

Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
            20                  25                  30

Asp Ser Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
        35                  40                  45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
    50                  55                  60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65                  70                  75                  80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
                85                  90                  95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
            100                 105                 110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
        115                 120                 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
    130                 135                 140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
145                 150                 155                 160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
                165                 170                 175
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```
Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
        180                 185             190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
        195                 200             205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
        210                 215             220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu
225             230             235             240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
            245             250             255

Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
        260             265             270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
        275             280             285

Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp
        290             295             300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys
305             310             315             320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
            325             330             335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val
        340             345             350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile
        355             360             365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile
        370             375             380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala
385             390             395             400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
            405             410             415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
            420             425             430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
            435             440             445

Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile
        450             455             460

Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
465             470             475
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<213> zea mays

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gctcatgata gtgttcttgg aatcattctg ggaggtggtg ctgggactag attgtacccc   180

ttgacaaaga agcgtgccaa gcctgcagtg ccattgggtg ccaactatag actgattgat   240

attcctgtca gcaattgtct caacagcaac atatccaaga tctatgtgct aacgcaattt   300

aactctgctt ccctcaaccg tcacctctca agagcctacg ggagcaacat tggagggtac   360

aagaatgaag ggtttgttga agtcttagct gcacagcaga gcccagataa tccaaactgg   420

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atggaatttc taattcttgc tggcgatcac ctgtaccgga tggactatga aaagttcatt   540

caggcacaca gagaaacaaa tgctgatatt accgttgctg ccctaccgat ggatgagaaa   600

cgtgcaactg catttggcct catgaaaatt gatgaagaag ggaggatcat tgagtttgct   660

gagaaaccga aaggagagca gttgaaagca atgatggttg acaccaccat acttggcctt   720

gatgacgtga gggcaaagga aatgccttat attgctagca tgggtatcta tgttttcagc   780

aaagatgtaa tgcttcagct cctccgtgaa caatttcctg aagccaatga ctttggaagt   840

gaggttattc caggtgcaac cagcattgga aagagggttc aggcttatct gtatgatggt   900

tactgggaag atatcggtac cattgcggca ttttataatg caaacttggg aataaccaag   960

aagccaatac cagatttcag cttctatgac cgttttgctc caatttatac acaacctcga   1020

cacctgccac cttcaaaggt tcttgatgct gatgtgacag acagtgttat tggtgaagga   1080

tgtgttatta aaaactgcaa gataaaccat tctgtagttg gactccgatc ttgcatatct   1140

gaaggtgcta tcatagagga cagtttacta atgggtgcgg actactatga gacagaagct   1200

gataaaaaac tccttgccga aaaaggtggc attcctattg gtattgggaa aaattcatgc   1260

atcaggagag caatcattga caagaatgct cgaattggag acaatgttaa gatactcaat   1320

gctgacaatg ttcaagaagc tgcaatggag acagacgggt acttcatcaa aggtggaatt   1380

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<213> zea mays

<400> 4

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1   5   10   15

Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
                20   25   30

Asp Ser Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
            35   40   45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
        50   55   60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65   70   75   80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
                85   90   95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
                100   105   110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
            115   120   125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
        130   135   140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
145   150   155   160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
                165   170   175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
                180   185   190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
            195   200   205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
        210   215   220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu
225   230   235   240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
                245   250   255

Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
        260   265   270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
        275   280   285

Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp
    290   295   300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys
305   310   315   320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
            325   330   335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val
        340   345   350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile
        355   360   365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile
    370   375   380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala
385   390   395   400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
            405   410   415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
            420   425   430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
        435   440   445

Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile
    450   455   460

Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
465   470   475

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cccttgacaa agaagcgtgc caagcctgca gtgccattgg gtgccaacta tagactgatt   240

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tacaagaatg aagggtttgt tgaagtctta gctgcacagc agagcccaga taatccaaac    420

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attcaggcac acagagaaac aaatgctgat attaccgttg ctgccctacc gatggatgag    600


aaacgtgcaa ctgcatttgg cctcatgaaa attgatgaag aagggaggat cattgagttt    660

gctgagaaac cgaaaggaga gcagttgaaa gcaatgatgg ttgacaccac catacttggc    720

cttgatgacg tgagggcaaa ggaaatgcct tatattgcta gcatgggtat ctatgttttc    780

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ggttactggg aagatatcgg taccattgcg gcatttttata atgcaaactt gggaataacc    960

aagaagccaa taccagattt cagcttctat gaccgttttg ctccaattta tacacaacct   1020

cgacacctgc caccttcaaa ggttcttgat gctgatgtga cagacagtgt tattggtgaa   1080

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gctgataaaa aactccttgc cgaaaaaggt ggcattccta ttggtattgg gaaaaattca   1260

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aatgctgaca atgttcaaga agctgcaatg gagacagacg ggtacttcat caaaggtgga   1380

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1               5                   10                  15


Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
            20                  25                  30


Asp Ser Gln Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
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Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
    50   55   60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
65   70   75   80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
                  85   90   95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
              100   105   110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
              115   120   125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
              130   135   140

Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn
145   150   155   160

Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp
              165   170   175

Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr
              180   185   190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu
              195   200   205

Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro
    210   215   220

Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly
225   230   235   240

Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly
              245   250   255

Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln
              260   265   270

Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr
              275   280   285

Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu
290   295   300

Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr
305   310   315   320

Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile
              325   330   335

Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp

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               340                     345                     350

Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
        355                     360                     365


Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala
    370                     375                     380


Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
385                     390                     395                 400


Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile
                405                     410                     415


Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
                420
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